

Sequence Listing

<110> KANNO, Sohei
 KIMURA, Eiichiro
 MATSUI, Kazuhiko
 NAKAMATSU, Tsuyoshi

<120> ABC Transporter and Gene Coding for the Same

<130> B-528SMOP924

<141> 1999-12-16

<150> JP 10-360621

<151> 1998-12-18

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (3,9,12)

<223> ~~n=a-or-c-or-g-or-t~~

<220>

<223> Description of Artificial Sequence:primer for
 amplifying Brevibacterium lactofermentum gltBD gene

<400> 1

ggngarggng gngarga

<210> 2
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1,4,7,)
 <223> n=a or c or g or t

<220>
 <223> Description of Artificial Sequence:primer for
 amplifying Brevibacterium lactofermentum gltBD gene

<400> 2
 nccncngtc atrtaytc 18

<210> 3
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer for
 amplifying Brevibacterium lactofermentum gltBD gene

<400> 3
 aatccacgtg aagctagtgg cagaacaagg cg 32

<210> 4
 <211> 30
 <212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer for
 amplifying Brevibacterium lactofermentum gltBD gene

<400> 4
 acgaatgaac aattcaccac tggttgcgcc 30

09868338.061801

<210> 5
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
 amplifying downstream region of gltBD gene

<400> 5
 atcctcgaca aggatctgtc cg

22

<210> 6
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
 amplifying downstream region of gltBD gene

<400> 6
 ggtttgtaa gtgtgccaag acagttgagc

30

<210> 7
 <211> 2370
 <212> DNA
 <213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(1101)

<220>

<221> CDS

<222> (1117)..(1725)

<220>

<221> CDS

<222> (1759)..(2367)

09868338.061801

<400> 7

atg ctg gcg acc cga cta att acc ttg ttc ttt ttc cta gga atc att	48
Met Leu Ala Thr Arg Leu Ile Thr Leu Phe Phe Phe Leu Gly Ile Ile	
1 5 10 15	
gga tcg cta acc ggt aac ctc agt gaa cta cgt gca caa act act ttt	96
Gly Ser Leu Thr Gly Asn Leu Ser Glu Leu Arg Ala Gln Thr Thr Phe	
20 25 30	
agt aca tta tgg gat acc cat aaa gaa acc tat aga gtc tcc ata gct	144
Ser Thr Leu Trp Asp Thr His Lys Glu Thr Tyr Arg Val Ser Ile Ala	
35 40 45	
tcc gca gca gga caa gac ttc tac ggg ctt gct gag act cta cgc act	192
Ser Ala Ala Gly Gln Asp Phe Tyr Gly Leu Ala Glu Thr Leu Arg Thr	
50 55 60	
atg gat agg cat ggg gaa att att ttg gca gat cgt caa tgg tta aca	240
Met Asp Arg His Gly Glu Ile Ile Leu Ala Asp Arg Gln Trp Leu Thr	
65 70 75 80	
gct ccc ctt gat atc ggt gca cca gtc gta tta tca aac aca act ttt	288
Ala Pro Leu Asp Ile Gly Ala Pro Val Val Leu Ser Asn Thr Thr Phe	
85 90 95	
gcc gtt gat gaa gga cta ctt gcg cca aaa gat cta ccg caa agt gac	336
Ala Val Asp Glu Gly Leu Leu Ala Pro Lys Asp Leu Pro Gln Ser Asp	
100 105 110	
gag atc aca ata ttg cat cct cag ttt ctg gat tcg gcc aaa gag cca	384
Glu Ile Thr Ile Leu His Pro Gln Phe Leu Asp Ser Ala Lys Glu Pro	
115 120 125	
gaa tta ctt ggt ttg ctg gag ttc gaa gca tcc aac tca caa gtg cca	432
Glu Leu Leu Gly Leu Leu Glu Phe Glu Ala Ser Asn Ser Gln Val Pro	
130 135 140	
atg cca aag atc caa agc att cca tat gat agc gaa gac tca acc aac	480
Met Pro Lys Ile Gln Ser Ile Pro Tyr Asp Ser Glu Asp Ser Thr Asn	
145 150 155 160	
ccc atg tct gaa gtt ttt acc tac aac att aac ctg gat agt gca gta	528
Pro Met Ser Glu Val Phe Thr Tyr Asn Ile Asn Leu Asp Ser Ala Val	
165 170 175	
aga aac cca atc gta gtt atc ctt ccc gca ggc tta gag ctt tta agt	576
Arg Asn Pro Ile Val Val Ile Leu Pro Ala Gly Leu Glu Leu Leu Ser	
180 185 190	
gat caa aat ttg tcg gct cga ctc aca cag aat agt ctg ctg ata aaa	624
Asp Gln Asn Leu Ser Ala Arg Leu Thr Gln Asn Ser Leu Leu Ile Lys	
195 200 205	
gac cag act ggt gtg aac gct ctt cta tcc tca gag gat tca cgc aat	672

Asp	Gln	Thr	Gly	Val	Asn	Ala	Leu	Leu	Ser	Ser	Glu	Asp	Ser	Arg	Asn	
210					215					220						
tat	gtg	gga	gct	gca	tcc	ccg	atg	att	gac	acg	tgg	gaa	gaa	agc	gtt	720
Tyr	Val	Gly	Ala	Ala	Ser	Pro	Met	Ile	Asp	Thr	Trp	Glu	Glu	Ser	Val	
225					230				235					240		
gtt	cgg	ttg	aag	gaa	gcg	aac	caa	ata	atc	gcc	ttc	aac	gct	ttc	att	768
Val	Arg	Leu	Lys	Glu	Ala	Asn	Gln	Ile	Ile	Ala	Phe	Asn	Ala	Phe	Ile	
				245					250					255		
gca	ttg	ttc	ctc	acg	acg	act	ctt	gtt	cta	gca	tac	tgc	act	ggt	att	816
Ala	Leu	Phe	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ala	Tyr	Cys	Thr	Gly	Ile	
				260					265					270		
tca	ttt	aag	aaa	tca	aag	aag	act	atg	ggt	agc	gca	tct	act	agg	aaa	864
Ser	Phe	Lys	Lys	Ser	Lys	Lys	Thr	Met	Gly	Ser	Ala	Ser	Thr	Arg	Lys	
				275				280						285		
tca	tcc	att	aag	agc	tcg	att	aca	gct	gct	aat	tgt	aga	agt	aat	ttt	912
Ser	Ser	Ile	Lys	Ser	Ser	Ile	Thr	Ala	Ala	Asn	Cys	Arg	Ser	Asn	Phe	
				290				295						300		
cgc	ttc	aat	tcc	gtg	cgt	ctg	gct	cgc	gaa	ccg	cta	ttt	cga	gcg	atc	960
Arg	Phe	Asn	Ser	Val	Arg	Leu	Ala	Arg	Glu	Pro	Leu	Phe	Arg	Ala	Ile	
305					310				315					320		
tgc	agc	aat	agc	ttc	aga	tgc	tcc	ctc	agc	cag	ata	ctt	aga	aca	tct	1008
Cys	Ser	Asn	Ser	Phe	Arg	Cys	Ser	Leu	Ser	Gln	Ile	Leu	Arg	Thr	Ser	
				325					330					335		
caa	ttc	tat	acc	tcc	atc	act	gcc	gtt	ggt	ttt	agg	aat	ctt	aat	aat	1056
Gln	Phe	Tyr	Thr	Ser	Ile	Thr	Ala	Val	Gly	Phe	Arg	Asn	Leu	Asn	Asn	
				340				345						350		
cgg	ttg	gac	ttc	act	ttc	att	ttt	cag	ttc	gat	gaa	gct	tcc	ttt		1101
Arg	Leu	Asp	Phe	Thr	Phe	Ile	Phe	Gln	Phe	Asp	Glu	Ala	Ser	Phe		
				355				360						365		
tgaaaagagc	acaca	atg	ata	gaa	atc	aat	gac	ctc	aag	aaa	tct	ttt	ggc			1152
					Met	Ile	Glu	Ile	Asn	Asp	Leu	Lys	Lys	Ser	Phe	Gly
					1				5					10		
gtt	cgg	atc	tta	tgg	caa	ggt	ctc	agt	cat	aag	ttt	tta	cca	gga	aca	1200
Val	Arg	Ile	Leu	Trp	Gln	Gly	Leu	Ser	His	Lys	Phe	Leu	Pro	Gly	Thr	
				15				20						25		
atg	aca	gca	ctg	act	gga	gcg	tcc	ggt	tca	gga	aaa	tcg	act	ttg	ctc	1248
Met	Thr	Ala	Leu	Thr	Gly	Ala	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	
				30				35						40		
aac	tgt	ctt	ggc	aca	ctt	gac	aaa	cca	agt	tcc	gga	cag	atc	ctt	gtc	1296
Asn	Cys	Leu	Gly	Thr	Leu	Asp	Lys	Pro	Ser	Ser	Gly	Gln	Ile	Leu	Val	
45					50						55				60	

00868338.061301

gag gat gta gac ctt ctg aaa ctc tct acg cgt aag caa cgg tta tac	1344
Glu Asp Val Asp Leu Leu Lys Leu Ser Thr Arg Lys Gln Arg Leu Tyr	
65 70 75	
agg aaa aat acg gtg ggc tat tta ttt caa gat tat gcc ttg att ccc	1392
Arg Lys Asn Thr Val Gly Tyr Leu Phe Gln Asp Tyr Ala Leu Ile Pro	
80 85 90	
gac agg aca gtt aaa ttc aac ctt cag ctt gcg gtg gaa aaa cac aaa	1440
Asp Arg Thr Val Lys Phe Asn Leu Gln Leu Ala Val Glu Lys His Lys	
95 100 105	
tgg cct gaa att cct caa gta ctt cat gct gtt ggt ctt gag tcg ttc	1488
Trp Pro Glu Ile Pro Gln Val Leu His Ala Val Gly Leu Glu Ser Phe	
110 115 120	
gag gaa aag cca gtt ttt gaa ctc tct ggt ggc gaa caa caa cga act	1536
Glu Glu Lys Pro Val Phe Glu Leu Ser Gly Gly Glu Gln Gln Arg Thr	
125 130 135 140	
gcg ttg gcc cgg gta ctg ctc aaa aat ccc cga ata att ctg gct gat	1584
Ala Leu Ala Arg Val Leu Leu Lys Asn Pro Arg Ile Ile Leu Ala Asp	
145 150 155	
gaa cca acc gga gct cta gat tta aca aac agt gag cta gtc ata gaa	1632
Glu Pro Thr Gly Ala Leu Asp Leu Thr Asn Ser Glu Leu Val Ile Glu	
160 165 170	
gca ttg aga gca ctc gcc gac aaa ggc gcc acc gtt gtt gtt gct acg	1680
Ala Leu Arg Ala Leu Ala Asp Lys Gly Ala Thr Val Val Val Ala Thr	
175 180 185	
cac tcg ccc ctc ttc cga gaa tca gcg gat acc att atc aaa cta	1725
His Ser Pro Leu Phe Arg Glu Ser Ala Asp Thr Ile Ile Lys Leu	
190 195 200	
taggtgcccc aacttttcgg agatctcagt gca atg atg gaa ttc tta aac act	1779
Met Met Glu Phe Leu Asn Thr	
1 5	
cac cgt ttg att gtt ctc ggg agt ttg tct ttt cta ggg cta ggt ttc	1827
His Arg Leu Ile Val Leu Gly Ser Leu Ser Phe Leu Gly Leu Gly Phe	
10 15 20	
gcg gaa gtc ctg ctg cgt ggc cag tgg tca aca ccg cag ttt ttt gtt	1875
Ala Glu Val Leu Leu Arg Gly Gln Trp Ser Thr Pro Gln Phe Phe Val	
25 30 35	
ttc act ttc ttg caa act ctg ctt ctc gta ttg tgt ttt att cct aaa	1923
Phe Thr Phe Leu Gln Thr Leu Leu Leu Val Leu Cys Phe Ile Pro Lys	
40 45 50 55	
ctc tcg gtt cct ttt gtg gtg ctt cta agc att gcc caa ctc gcg ctt	1971
Leu Ser Val Pro Phe Val Val Leu Leu Ser Ile Ala Gln Leu Ala Leu	

09868338 "061301

<210> 8

<212> PRT

<400> 8

Met Leu Ala Thr Arg Leu Ile Thr Leu Phe Phe Phe Leu Gly Ile Ile
1 5 10 15
Gly Ser Leu Thr Gly Asn Leu Ser Glu Leu Arg Ala Gln Thr Thr Phe
20 25 30
Ser Thr Leu Trp Asp Thr His Lys Glu Thr Tyr Arg Val Ser Ile Ala
35 40 45

Ser Ala Ala Gly Gln Asp Phe Tyr Gly Leu Ala Glu Thr Leu Arg Thr
 50 55 60
 Met Asp Arg His Gly Glu Ile Ile Leu Ala Asp Arg Gln Trp Leu Thr
 65 70 75 80
 Ala Pro Leu Asp Ile Gly Ala Pro Val Val Leu Ser Asn Thr Thr Phe
 85 90 95
 Ala Val Asp Glu Gly Leu Leu Ala Pro Lys Asp Leu Pro Gln Ser Asp
 100 105 110
 Glu Ile Thr Ile Leu His Pro Gln Phe Leu Asp Ser Ala Lys Glu Pro
 115 120 125
 Glu Leu Leu Gly Leu Leu Glu Phe Glu Ala Ser Asn Ser Gln Val Pro
 130 135 140
 Met Pro Lys Ile Gln Ser Ile Pro Tyr Asp Ser Glu Asp Ser Thr Asn
 145 150 155 160
 Pro Met Ser Glu Val Phe Thr Tyr Asn Ile Asn Leu Asp Ser Ala Val
 165 170 175
 Arg Asn Pro Ile Val Val Ile Leu Pro Ala Gly Leu Glu Leu Leu Ser
 180 185 190
 Asp Gln Asn Leu Ser Ala Arg Leu Thr Gln Asn Ser Leu Leu Ile Lys
 195 200 205
 Asp Gln Thr Gly Val Asn Ala Leu Leu Ser Ser Glu Asp Ser Arg Asn
 210 215 220
 Tyr Val Gly Ala Ala Ser Pro Met Ile Asp Thr Trp Glu Glu Ser Val
 225 230 235 240
 Val Arg Leu Lys Glu Ala Asn Gln Ile Ile Ala Phe Asn Ala Phe Ile
 245 250 255
 Ala Leu Phe Leu Thr Thr Thr Leu Val Leu Ala Tyr Cys Thr Gly Ile
 260 265 270
 Ser Phe Lys Lys Ser Lys Lys Thr Met Gly Ser Ala Ser Thr Arg Lys
 275 280 285
 Ser Ser Ile Lys Ser Ser Ile Thr Ala Ala Asn Cys Arg Ser Asn Phe
 290 295 300

 Arg Phe Asn Ser Val Arg Leu Ala Arg Glu Pro Leu Phe Arg Ala Ile
 305 310 315 320
 Cys Ser Asn Ser Phe Arg Cys Ser Leu Ser Gln Ile Leu Arg Thr Ser
 325 330 335
 Gln Phe Tyr Thr Ser Ile Thr Ala Val Gly Phe Arg Asn Leu Asn Asn
 340 345 350
 Arg Leu Asp Phe Thr Phe Ile Phe Gln Phe Asp Glu Ala Ser Phe
 355 360 365

09868338 "0618001

<210> 9
 <211> 203
 <212> PRT
 <213> Brevibacterium lactofermentum

<400> 9
 Met Ile Glu Ile Asn Asp Leu Lys Lys Ser Phe Gly Val Arg Ile Leu
 1 5 10 15
 Trp Gln Gly Leu Ser His Lys Phe Leu Pro Gly Thr Met Thr Ala Leu
 20 25 30
 Thr Gly Ala Ser Gly Ser Gly Lys Ser Thr Leu Leu Asn Cys Leu Gly
 35 40 45
 Thr Leu Asp Lys Pro Ser Ser Gly Gln Ile Leu Val Glu Asp Val Asp
 50 55 60
 Leu Leu Lys Leu Ser Thr Arg Lys Gln Arg Leu Tyr Arg Lys Asn Thr
 65 70 75 80
 Val Gly Tyr Leu Phe Gln Asp Tyr Ala Leu Ile Pro Asp Arg Thr Val
 85 90 95
 Lys Phe Asn Leu Gln Leu Ala Val Glu Lys His Lys Trp Pro Glu Ile
 100 105 110
 Pro Gln Val Leu His Ala Val Gly Leu Glu Ser Phe Glu Glu Lys Pro
 115 120 125
 Val Phe Glu Leu Ser Gly Gly Glu Gln Gln Arg Thr Ala Leu Ala Arg
 130 135 140
 Val Leu Leu Lys Asn Pro Arg Ile Ile Leu Ala Asp Glu Pro Thr Gly
 145 150 155 160
 Ala Leu Asp Leu Thr Asn Ser Glu Leu Val Ile Glu Ala Leu Arg Ala
 165 170 175
 Leu Ala Asp Lys Gly Ala Thr Val Val Val Ala Thr His Ser Pro Leu
 180 185 190
 Phe Arg Glu Ser Ala Asp Thr Ile Ile Lys Leu
 195 200

<210> 10
 <211> 203
 <212> PRT
 <213> Brevibacterium lactofermentum

<400> 10
 Met Met Glu Phe Leu Asn Thr His Arg Leu Ile Val Leu Gly Ser Leu
 1 5 10 15

09868338-061801

Ser Phe Leu Gly Leu Gly Phe Ala Glu Val Leu Leu Arg Gly Gln Trp
 20 25 30
 Ser Thr Pro Gln Phe Phe Val Phe Thr Phe Leu Gln Thr Leu Leu Leu
 35 40 45
 Val Leu Cys Phe Ile Pro Lys Leu Ser Val Pro Phe Val Val Leu Leu
 50 55 60
 Ser Ile Ala Gln Leu Ala Leu Ala Tyr Leu Cys Ile His Gly Glu Pro
 65 70 75 80
 Gln Ser Thr Ser Pro Phe Thr Leu Ile Val Ala Gln Met Ala Phe Ser
 85 90 95
 Gly Leu Leu Met Phe Arg Gly Gln Arg Val Leu Ala Phe Ile Ser Ala
 100 105 110
 Gly Gly Leu Ile Trp Ile Gly Thr Ile Asp Pro Thr Asn Gly Ala Trp
 115 120 125
 Ser Pro His Val Met Ser Ala Leu Ala Leu Ala Val Phe Phe Ala Leu
 130 135 140
 Ser Met Ala Leu Gly Gln Val Leu Arg Ser Lys Val Glu Gln Arg Ala
 145 150 155 160
 Asn Leu Glu Glu Gln Ala Lys Ile Gln Thr Glu Leu Arg Arg Lys Glu
 165 170 175
 Leu Ser Thr Pro Ser Ala Ser Val Gly Cys Gln Arg Thr Tyr Val Cys
 180 185 190
 Ser Asp Glu Ile Ala Gly Ala Gln Trp Ser Arg
 195 200

09868338 061801